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C3
1. (Once Amended) A method of selecting and/or identifying one or more protein affinity ligands, wherein the affinity ligands are antibodies, that bind to one or more proteins of interest, comprising the steps of:

(A) obtaining a real or theoretical mass spectrometry based characterization of the one or more proteins by either:

i. Subjecting the one or more proteins to a mass spectrometry based characterization; or

ii. Predicting the mass spectrometry based characterization from known data;

(B) utilising the one or more proteins either individually or as a mixture to:

i. Generate one or more antibodies thereto by immunisation; and/or

ii. Select, using a single or multiple rounds of binding, one or more antibodies thereto;

(C) screening the one or more antibodies generated in step B(i) and/or the one or more antibodies selected in step (B)(ii) by:

i. adding the one or more proteins individually or as a mixture of proteins to the one or more antibodies generated in step (B)(i) or the one or more antibodies selected in step (B)(ii), each antibody being used individually, and

ii. after removing any proteins which have not bound, eluting the at least one protein that has bound;

(D) subjecting the at least one eluted protein to a mass spectrometry based characterization; and

(E) by comparing the mass spectrometry based characterization obtained in steps (A) and (D), selecting and/or identifying the at least one antibody that binds to the one or more proteins of interest.

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15. (Once amended) A method of screening an antibody to a protein characterised in that the antibody is generated or selected using an impure protein or a complex protein mixture and then identified by comparing a mass spectrometry based characterization obtained from the protein/proteins for which it is specific with that of a mass spectrometry based characterization which is theoretical for said protein/proteins or is obtained from the impure protein or complex protein mixture.

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16. (Once amended) A method of selecting an antibody specific to a given peptide characterised in that the antibody is selected by comparing a mass spectrometry based characterization of the protein/proteins released from the antibody to which it binds with a mass spectrometry based characterization which is theoretical for said protein/proteins or is obtained from the known protein.

31. (New) The method of claim 1 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

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32. (New) The method of claim 15 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

33. (New) The method of claim 16 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

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~~34. (New) A method of selecting and/or identifying at least one antibody which binds at least one protein of interest, comprising the steps of:~~

- ~~(A) obtaining a pre-selected mass spectrometry-based characterization of a target protein to serve as a reference standard;~~
- ~~(B) providing an antibody which selectively binds to said target protein;~~
- ~~(C) isolating and collecting said target protein through affinity binding with said antibody;~~
- ~~(D) analyzing said collected target protein for said pre-selected mass spectrometry-based characterization; and~~
- ~~(E) comparing the mass spectrometry-based characterization obtained in step (D) with the reference standard of step (A).~~

35. (New) The method of selecting and/or identifying at least one antibody which binds at least one protein of interest recited in claim 34 wherein said mass spectrometry-based characterization is a peptide mass fingerprint.

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cont.

36. (New) The method of claim 35, further comprising the step of obtaining an additional mass spectrometry-based characterization in addition to said peptide mass fingerprint.
